

DOCKET NO.: IBIS0035-101 (IBIS-0012)

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Amendments to the claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

Claims 1-26 (canceled).

Claim 27 (previously presented): An oligonucleotide comprising a molecular interaction site that is present in prokaryotic RNA and in at least one additional prokaryotic RNA, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said prokaryotic RNA, wherein the binding of said molecule to said molecular interaction site does not modulate translation of said RNA.

Claim 28 (previously presented): The oligonucleotide of claim 27 wherein said molecular interaction site is not present in eukaryotic RNA.

Claim 29 (previously presented): The oligonucleotide of claim 27 wherein said molecular interaction site is not present in human RNA.

Claims 30-34 (canceled).

Claim 35 (currently amended): An oligonucleotide comprising a molecular interaction site that is present in the RNA of a selected organism and in the RNA of at least one additional organism, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said RNA in said selected organism, wherein said oligonucleotide does not comprise the an iron response element, wherein said molecular interaction site is identified by a method comprising:

comparing the nucleotide sequence of said RNA of a selected organism with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species;

identifying at least one sequence region which is conserved among said plurality of nucleic acids and said RNA of a selected organism;

determining whether said conserved region has secondary structure; and

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for said conserved region having secondary structure, identifying said secondary structure.

Claim 36 (previously presented): The oligonucleotide of claim 35 wherein said method further comprises identifying at least one structural motif for said conserved region having secondary structure.

Claim 37 (previously presented): The oligonucleotide of claim 36 wherein said method further comprises constructing a set of descriptor elements for said structural motif.

Claim 38 (previously presented): The oligonucleotide of claim 37 wherein said method further comprises identifying further nucleic acids having secondary structures corresponding to said descriptor elements.

Claim 39 (previously presented): The oligonucleotide of claim 35 wherein said RNA of a selected organism is present in a eukaryotic cell.

Claim 40 (previously presented): The oligonucleotide of claim 39 wherein said RNA of a selected organism is selected from the group consisting of mRNA, pre-mRNA, tRNA, rRNA, and snRNA.

Claim 41 (previously presented): The oligonucleotide of claim 35 wherein said RNA of a selected organism is present in a prokaryotic cell.

Claim 42 (canceled).

Claim 43 (previously presented): The oligonucleotide of claim 35 further comprising comparing said RNA of a selected organism to paralogous nucleic acids.

Claim 44 (previously presented): The oligonucleotide of claim 35 wherein said plurality of nucleic acids from different taxonomic species is obtained by performing a sequence similarity search, an ortholog search, or a combination thereof.

Claim 45 (previously presented): The oligonucleotide of claim 35 wherein said plurality of nucleic acids from different taxonomic species is obtained by performing a sequence similarity search and constructing virtual transcripts.

Claim 46 (previously presented): The oligonucleotide of claim 35 wherein determining whether said conserved region has secondary structure is performed by self complementarity comparison, alignment and covariance analysis, secondary structure prediction, or a combination thereof.

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Claim 47 (previously presented): The oligonucleotide of claim 46, wherein said secondary structure comprises at least one bulge, loop, stem, hairpin, knot, triple interact, cloverleaf, or helix.

Claim 48 (previously presented): The oligonucleotide of claim 36 wherein said structural motif is identified by performing self complementarity comparison, alignment and covariance analysis, secondary structure prediction, or a combination thereof.

Claim 49 (previously presented): The oligonucleotide of claim 37 wherein said set of descriptor elements is constructed using a descriptor database.

Claim 50 (previously presented): The oligonucleotide of claim 38 wherein said other nucleic acids having secondary structures corresponding to said descriptor elements are identified by searching at least one database, performing clustering and analysis, searching for orthologs, or a combination thereof.

Claim 51 (currently amended): An oligonucleotide comprising a molecular interaction site that is present in the RNA of a selected organism and in the RNA of at least one additional organism, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said RNA in said selected organism, wherein said oligonucleotide does not comprise the-an iron response element, wherein said molecular interaction site is identified by a method comprising:

comparing the nucleotide sequence of said RNA of a selected organism with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species, wherein said nucleotide sequence of said RNA of a selected organism is determined by assembling a plurality of expressed sequence tags;

identifying at least one sequence region which is conserved among said plurality of nucleic acids and said RNA of a selected organism;

determining whether said conserved region has secondary structure; and

for said conserved region having secondary structure, identifying said secondary structure.

Claim 52 (currently amended): An oligonucleotide comprising a molecular interaction site that is present in the RNA of a selected organism and in the RNA of at least one additional organism, wherein said molecular interaction site serves as a binding site for at least one molecule that when

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bound to said molecular interaction site modulates the expression of said RNA in said selected organism, wherein said oligonucleotide does not comprise ~~the an~~ iron response element or ~~the a~~ 3' untranslated region of ~~the a~~ histone mRNA, wherein said molecular interaction site is identified by a method comprising:

comparing the nucleotide sequence of said RNA of a selected organism with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species;

identifying at least one sequence region which is conserved among said plurality of nucleic acids and said RNA of a selected organism;

determining whether said conserved region has secondary structure; and

for said conserved region having secondary structure, identifying said secondary structure.

Claim 53 (previously presented): The oligonucleotide of claim 52 wherein said method further comprises identifying at least one structural motif for said conserved region having secondary structure.

Claim 54 (previously presented): The oligonucleotide of claim 53 wherein said method further comprises constructing a set of descriptor elements for said structural motif.

Claim 55 (previously presented): The oligonucleotide of claim 54 wherein said method further comprises identifying further nucleic acids having secondary structures corresponding to said descriptor elements.

Claim 56 (previously presented): The oligonucleotide of claim 52 wherein said RNA of a selected organism is present in a eukaryotic cell.

Claim 57 (previously presented): The oligonucleotide of claim 56 wherein said RNA of a selected organism is selected from the group consisting of mRNA, pre-mRNA, tRNA, rRNA, and snRNA.

Claim 58 (previously presented): The oligonucleotide of claim 52 wherein said RNA of a selected organism is present in a prokaryotic cell.

Claim 59 (previously presented): The oligonucleotide of claim 52 further comprising comparing said RNA of a selected organism to paralogous nucleic acids.

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Claim 60 (previously presented): The oligonucleotide of claim 52 wherein said plurality of nucleic acids from different taxonomic species is obtained by performing a sequence similarity search, an ortholog search, or a combination thereof.

Claim 61 (previously presented): The oligonucleotide of claim 52 wherein said plurality of nucleic acids from different taxonomic species is obtained by performing a sequence similarity search and constructing virtual transcripts.

Claim 62 (previously presented): The oligonucleotide of claim 52 wherein determining whether said conserved region has secondary structure is performed by self complementarity comparison, alignment and covariance analysis, secondary structure prediction, or a combination thereof.

Claim 63 (previously presented): The oligonucleotide of claim 62, wherein said secondary structure comprises at least one bulge, loop, stem, hairpin, knot, triple interact, cloverleaf, or helix.

Claim 64 (previously presented): The oligonucleotide of claim 53 wherein said structural motif is identified by performing self complementarity comparison, alignment and covariance analysis, secondary structure prediction, or a combination thereof.

Claim 65 (previously presented): The oligonucleotide of claim 54 wherein said set of descriptor elements is constructed using a descriptor database.

Claim 66 (previously presented): The oligonucleotide of claim 55 wherein said other nucleic acids having secondary structures corresponding to said descriptor elements are identified by searching at least one database, performing clustering and analysis, searching for orthologs, or a combination thereof.

Claim 67 (currently amended): An oligonucleotide comprising a molecular interaction site that is present in the RNA of a selected organism and in the RNA of at least one additional organism, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said RNA in said selected organism, wherein said oligonucleotide does not comprise ~~the~~ an iron response element or ~~the~~ a 3' untranslated region of ~~the~~ a histone mRNA, wherein said molecular interaction site is identified by a method comprising:

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comparing the nucleotide sequence of said RNA of a selected organism with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species, wherein said nucleotide sequence of said RNA of a selected organism is determined by assembling a plurality of expressed sequence tags;

identifying at least one sequence region which is conserved among said plurality of nucleic acids and said RNA of a selected organism;

determining whether said conserved region has secondary structure; and

for said conserved region having secondary structure, identifying said secondary structure.